1

Appendix 2: CLUSTAL W (1.83) multiple sequence alignment

```
043759_SYNGR1a      MEGGAYGAGKAG-GAFDPYTLVRQPHTILRVVSWLFSIVVFGSIVNEGYLNSASEGEEFC
043759_SYNGR1b      MEGGAYGAGKAG-GAFDPYTLVRQPHTILRVVSWLFSIVVFGSIVNEGYLNSASEGEEFC
043759_SYNGR1c      MLTLEFGILEFDPSWIGSWTQRSWVSWRSRPGCELFSIVVFGSIVNEGYLNSASEGEEFC
SEQ_ID_297          MEGGAYGAGKAG-GAFDPYTLVRQPHTILRVVSWLFSIVVFGSIVNEGYLNSASEGEQFC
                    +++++++++++++ ++++                 ***************************:

043759_SYNGR1a      IYNRNPNACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKKAVLSDIGVSAFWAFLW
043759_SYNGR1b      IYNRNPNACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKKAVLSDIGVSAFWAFLW
043759_SYNGR1c      IYNRNPNACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKKAVLSDIGVSAFWAFLW
SEQ_ID_297          IYNRNPNACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKKAVLSDIGVSSPHRAG
                    ********:***********************************************

043759_SYNGR1a      FVGFCYLANQWQVSKPKDNPLNEGTDAARAAIAFSFFSIFTWAGQAVLAFQRYQIGADSA
043759_SYNGR1b      FVGFCYLANQWQVSKPKDNPLNEGTDAARAAIAFSFFSIFTWSLTAALAVRRFKDLSFQE
043759_SYNGR1c      FVGFCYLANQWQVSKPKDNPLNEGTDAARAAIAFSFFSIFTWSLTAALAVRRFKDLSFQE
SEQ_ID_297          RPRLSDECGFGR------------------------------------------------

043759_SYNGR1a      LFSQDYMDPSQDSSMPYAPYVEPNTGPDPAGMGGTYQQPANTFDTEPQGYQSQGY
043759_SYNGR1b      EYSTLFPASAQP-------------------------------------------
043759_SYNGR1c      EYSTLFPASAQP-------------------------------------------
SEQ_ID_297          -------------------------------------------------------
```